



1600

RAW SEQUENCE LISTING

DATE: 10/30/2002

PATENT APPLICATION: US/09/853,257A

TIME: 13:03:56

Input Set : A:\PUNIV.002A.TXT

Output Set: N:\CRF4\10292002\I853257A.raw

4 <110> APPLICANT: Bonnie L. Bassler
 5 Brendan N. Lilley
 7 <120> TITLE OF INVENTION: LUXO-SIGMA54 INTERACTIONS AND METHODS OF
 8 USE
 10 <130> FILE REFERENCE: PUNIV.002A
 12 <140> CURRENT APPLICATION NUMBER: 09/853,257A
 13 <141> CURRENT FILING DATE: 2001-05-10
 15 <150> PRIOR APPLICATION NUMBER: 60/202,999
 16 <151> PRIOR FILING DATE: 2000-05-10
 18 <160> NUMBER OF SEQ ID NOS: 19
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 4003
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Vibrio harveyi
 27 <400> SEQUENCE: 1

ENTERED

28 agctcacggt ctttcattgc catacgggaa ttccatatac agcacatacg caccagtgcg 60
 29 ggtatggcac tatcaggtgg tgaacgcgcg cgtgtagaaa ttgctcgtgc attgjcagca 120
 30 aaccctcagt tcatttttgt ggatgaacgc ttgcgggtg ttgacccaat ttcggttaac 180
 31 gacatcaaaa aaatcatcga acacttgccg gatcgcgcc ttggcgtgtt aatcacagac 240
 32 cataacgtac gcgaaacctt ggaagtttgt gaaaaagcct atatcgtaag ccaaggacac 300
 33 ctcatcgcat cgggaactcc ggatgaagtt ctcaataacg agcaagtga acaagtttat 360
 34 ctgcggcaac aattcogtct atgattacat taaggaacggt aagattctga gcattacaag 420
 35 gtaagtaaca ctgaatgaaa ccttcattac aactcaagct aggtcaacag ttagccatga 480
 36 cgccacagct cgagcaagcg attcgtttgt tgaattgtc gacgctcgat cttcaacaag 540
 37 aaatccaaga agcgttggac tccaaacgcg tactggaagt tgaagaaggc cagcatgagc 600
 38 ctcaagcaaa tggatgaagc aaatcagcgt ctgaattctg tgataaaaagt gcgaacgaag 660
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 40 tcagctctga cctagaaatt gatacaactt gggatgaagt atatagcgca aacacgggca 780
 41 gcacaggcct agcgtctgat gatgacatgc cgtctacca aggtgagacc actgaattct 840
 42 tgcattgatta cttatgttgg cagtttagct taacgccttt cagtgaacac gaccgcacca 900
 43 tcgcctcgcg gattatcgat ggggtcgacg actacggcta cttaacctc tccctgaag 960
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 45 agcgtattca gcaatttgac ccgctcgggt tagcctctcg caatctgcaa gaatgcctac 1080
 46 tgctacaaat ggcaactttc cctgaagaca cgcgctggct tgctgagggc aaaatggtgt 1140
 47 tgaagatca cctgacccac cttgggaatc ctgactacaa gctggtcctc aaagagccta 1200
 48 agcttaaaaga agcggacttg cgtgaagtat tgaagttgat tcaacaactt gaccacagtc 1260
 49 caggtagtcg tatcaacacc gatgacactg aatacgtcat tccggatgtg tccgtattta 1320
 50 aaqatcatgg taagtggacc gtctccataa accctgacag cattedcgaaa ctaaaagtta 1380
 51 atcaacaata tgcgcaacta ggcaaaaggca acagtgcgga tagccaglac attcgcagca 1440
 52 atttgcaaga ggcaaaatgg ctgattaaga gactagaaag cagaaaagag acgcttctca 1500
 53 aagttgcaag atgtatttgt caacatcaac aagatttctt cgagtatggt gaagaagcca 1560
 54 tgaaccaaat ggtgctaaac gacgtagcat tggatgtgga catgcatgaa tcgacaattt 1620

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55 ctcgtgtaac aacacagaag tttatgcata ccccaoctgq catttttgaa ttgaagtact 1680
56 tcttctctag coatgttagt acagacaatg gtggagagtg ttcgtccaca gcaattcgcg 1740
57 cactcatcaa aaagtgtgtc gcagcggaga ataccgctaa gccactgagt gatagcaaaa 1800
58 ttgctgctct tctggctgac caggggattc aagtcgcgag acggacgata gcaaaatctc 1860
59 gtgaatcctt ggttattgcc ccttcgagtc agcgtaaaag cctactttag gcaccaattg 1920
60 aaaaggaaaag tctatgcaaa tcaatattea aggccatcac gttgatctta ccgattcaat 1980
61 gcaagaatat gttgactcta agttttcaaaa gctcgagcgg ttcttcgacc acatcaatca 2040
62 agtccatgtc gtattaaaaa ttgaaaaact taaccaaata gccgaagcta cgtccacatc 2100
63 caatcaaggc gaaatccacy cgtcatcgaa cgaagaaagt atgtatgcag caattgatct 2160
64 gctggtggat aaattagtgc gtcaacttaa caagcacaaa gaaaaactaa acagtcatca 2220
65 atcatgcaat ttagcgaaat actgtcactg gaactgcaaa aaagtgggtt ccatgtaca 2280
66 agtaagaaac gtgccttcga aatgatcagc caaattgtcg ctgaaaacac gggccaagat 2340
67 tctacagaac tgtttgagtg tatgctcagc agagaaaaaa tgggtagtag tggtatcggc 2400
68 aacggtattg ctatccctca cgaagaatg caatcaaggc acaaagccat cgcagtgtta 2460
69 cttcagtggt acgaagcaat tgaatttgac gctatcgaca accgacctgt cgacctctt 2520
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71 gcagagcgtc taagtgcaca gcaagtgtct aaaagcttac gtaacgctca gagcgatgaa 2640
72 gagctctacg acattatgat tcataagtaa tcaggacgat caccatgcga ttaatcgttg 2700
73 ttacgggcca ctctggtgcc gggaaaagtg ttgcctcgcg cgtacttgag gacttaggtt 2760
74 actactcgct agacaacctc cgggtaaaact tcttgacgc gtttgttcag tcagtctctg 2820
75 agagcaaaaca aaatgtcgca gtaagcatcg atattcgaaa tatccctaag aagctcaaa 2880
76 aactgaatac cactctagag aagctaaagg ctgaaactga tgtgacagta ctgttcttag 2940
77 acgcaataaa agaaacgctt ctcaccgct acagcgaaac acgtcggatt caccgctat 3000
78 cacttgacag tcaatcatca tcaattgac aggcgattga gcttgaaaca gagatcttaa 3060
79 tgcctctgaa agcacacgca gaattagtct tgaacagtag cggtaaatct ctgcatgac 3120
80 tcagtgaaac cgtacgtatg cgtgtggaag gcgagaaacg caaagactta gtcattggt 3180
81 ttgagtcggt tggtttcaaa tacggtttac caccagatgc cgtattcgtg tttgatgtgc 3240
82 gtttcttgcc aaacccacac tgggagccag cactgcgcgc tctcactggt ttagatggcc 3300
83 cgatcggcgc cttcttagag caacaccagt cggtaactga tctgaaatac caaattgaaa 3360
84 gctttattga gaattggtta ccactattag agaaaaacaa ccgtagttaa ctgaccgttg 3420
85 cgattggttg tactggtggt aaacaccgct cggtttatct tactcaaaaa attggtgagt 3480
86 tctttgcgga caaaggacac caagtacaaa ttgcacacac ttcattggaa aagaacgtta 3540
87 aggaataacg gtggaattaa gtcgtaaagt actgatccaa aaccgactag gcttgacgc 3600
88 tcgtgcggca gttaaaactg tagaactagc acaaagcttc gacgcggtga ttaccatcga 3660
89 caacgaagaa gacaaaaacg cgaaccgaga cagcgtcatg ggattgctga tgcgtgaatc 3720
90 agcccaagga caatacgtga ccaccacgc cactggcgat caatctgagc aagctcttga 3780
91 tgcggtttgc catctgacg agataagtt tgacgaaggc gattgattca ctgcctttt 3840
92 tattatctct agccagatat ccacataaa tttcacctcc tctttaaatt ccgacaaata 3900
93 attttgtcga ctctcataag ttgttattaa aaggtgccta gaattaagtt attattcaaa 3960
94 caattgtaaa tatcaggaat tgggaggaat gaatggcaga gca 4003

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96 <210> SEQ ID NO: 2

97 <211> LENGTH: 491

98 <212> TYPE: PRT

99 <213> ORGANISM: Vibrio harveyi

101 <400> SEQUENCE: 2

102 Met Lys Pro Ser Leu Gln Leu Lys Leu Gly Gln Gln Leu Ala Met Thr

103 1 5 10 15

104 Pro Gln Leu Gln Gln Ala Ile Arg Leu Leu Gln Leu Ser Thr Leu Asp

105 20 25 30

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106 Leu Gln Gln Glu Ile Gln Glu Ala Leu Asp Ser Asn Pro Leu Leu Glu
107          35          40          45
108 Val Glu Glu Gly His Asp Glu Pro Gln Ala Asn Gly Glu Asp Lys Ser
109          50          55          60
110 Ala Ser Glu Ser Ala Asp Lys Ser Ala Asn Glu Ala Asn Asp Ala Ser
111 65          70          75          80
112 Glu Pro Asp Leu Pro Asp Ser Ser Asp Val Ile Glu Lys Ser Glu Ile
113          85          90          95
114 Ser Ser Glu Leu Glu Ile Asp Thr Thr Trp Asp Asp Val Tyr Ser Ala
115          100          105          110
116 Asn Thr Gly Ser Thr Gly Leu Ala Leu Asp Asp Asp Met Pro Val Tyr
117          115          120          125
118 Gln Gly Glu Thr Thr Glu Ser Leu His Asp Tyr Leu Met Trp Gln Leu
119          130          135          140
120 Asp Leu Thr Pro Phe Ser Glu Thr Asp Arg Thr Ile Ala Leu Ala Ile
121 145          150          155          160
122 Ile Asp Ala Val Asp Asp Tyr Gly Tyr Leu Thr Leu Ser Pro Glu Glu
123          165          170          175
124 Ile His Glu Ser Phe Asp Asn Glu Glu Val Glu Leu Asp Glu Val Glu
125          180          185          190
126 Ala Val Arg Lys Arg Ile Gln Gln Phe Asp Pro Leu Gly Val Ala Ser
127          195          200          205
128 Arg Asn Leu Gln Glu Cys Leu Leu Leu Gln Leu Ala Thr Phe Pro Glu
129          210          215          220
130 Asp Thr Pro Trp Leu Ala Glu Ala Lys Met Val Leu Ser Asp His Ile
131 225          230          235          240
132 Asp His Leu Gly Asn Arg Asp Tyr Lys Leu Val Ile Lys Glu Ala Lys
133          245          250          255
134 Leu Lys Glu Ala Asp Leu Arg Glu Val Leu Lys Leu Ile Gln Gln Leu
135          260          265          270
136 Asp Pro Arg Pro Gly Ser Arg Ile Thr Pro Asp Asp Thr Glu Tyr Val
137          275          280          285
138 Ile Pro Asp Val Ser Val Phe Lys Asp His Gly Lys Trp Thr Val Ser
139          290          295          300
140 Ile Asn Pro Asp Ser Ile Pro Lys Leu Lys Val Asn Gln Gln Tyr Ala
141 305          310          315          320
142 Gln Leu Gly Lys Gly Asn Ser Ala Asp Ser Gln Tyr Ile Arg Ser Asn
143          325          330          335
144 Leu Gln Glu Ala Lys Trp Leu Ile Lys Ser Leu Glu Ser Arg Asn Glu
145          340          345          350
146 Thr Leu Leu Lys Val Ala Arg Cys Ile Val Glu His Gln Gln Asp Phe
147          355          360          365
148 Phe Glu Tyr Gly Glu Glu Ala Met Lys Pro Met Val Leu Asn Asp Val
149          370          375          380
150 Ala Leu Asp Val Asp Met His Glu Ser Thr Ile Ser Arg Val Thr Thr
151 385          390          395          400
152 Gln Lys Phe Met His Thr Pro Arg Gly Ile Phe Glu Leu Lys Tyr Phe
153          405          410          415
154 Phe Ser Ser His Val Ser Thr Asp Asn Gly Gly Glu Cys Ser Ser Thr

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155          420          425          430
156 Ala Ile Arg Ala Leu Ile Lys Lys Leu Val Ala Ala Glu Asn Thr Ala
157          435          440          445
158 Lys Pro Leu Ser Asp Ser Lys Ile Ala Ala Leu Leu Ala Asp Gln Gly
159          450          455          460
160 Ile Gln Val Ala Arg Arg Thr Ile Ala Lys Tyr Arg Glu Ser Leu Gly
161 465          470          475          480
162 Ile Ala Pro Ser Ser Gln Arg Lys Arg Leu Leu
163          485          490
166 <210> SEQ ID NO: 3
167 <211> LENGTH: 476
168 <212> TYPE: DNA
169 <213> ORGANISM: Vibrio harveyi
171 <400> SEQUENCE: 3
172 atgaaacctt cattacaact caagctaggt caacagttag ccatgacgcc acagctgcag 60
173 caagcgattc gtttggttga attgtcgacg ctgatcttc aacaagaaat ccaagaagcg 120
174 ttggactcca acccgctact ggaagttgaa gaaggccacg atgagcctca agcaaattgt 180
175 aaagacaaat cagcgtctga atctgctgat aaaagtgcga acgaagctaa cgatgctca 240
176 gaaccgcacc ttccagatag ctcgacgtg attgaaaaat ctgaaatcag ctctgagcta 300
177 gaaattgata ccacttggga tgacgtatat agcgcaaaca cgggcagcac aggcctagcg 360
178 ctggatgatg acatgcccggt ctaccaaggt gagaccactg aatctttgca tgattacctt 420
179 atgtgcagtg tagacttaac gcctttcagt gaaaccgacc gcaccatcgc cctcgc 476
181 <210> SEQ ID NO: 4
182 <211> LENGTH: 6
183 <212> TYPE: PRT
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: portion of consensus sequence of sigma-54 domains
W--> 189 <221> NAME/KEY: VARIANT
190 <222> LOCATION: (1)...(6)
191 <223> OTHER INFORMATION: Xaa = Trp or Phe
W--> 193 <400> 4
W--> 194 Xaa Phe Pro Gly Asn Val
195 1 5
198 <210> SEQ ID NO: 5
199 <211> LENGTH: 6
200 <212> TYPE: PRT
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: portion of consensus sequence of sigma-54 domains
W--> 206 <221> NAME/KEY: VARIANT
207 <222> LOCATION: (1)...(6)
208 <223> OTHER INFORMATION: Xaa = Val, Ala, Asp, Glu, Gly
W--> 210 <400> 5
W--> 211 Glu Leu Phe Gly His Xaa
212 1 5
215 <210> SEQ ID NO: 6
216 <211> LENGTH: 20
217 <212> TYPE: DNA

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218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <223> OTHER INFORMATION: upstream primer to amplify rpoN gene
223 <400> SEQUENCE: 6
224 qqycaacart tagcsatgac 20
226 <210> SEQ ID NO: 7
227 <211> LENGTH: 21
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: downstream primer to amplify rpoN gene
234 <400> SEQUENCE: 7
235 cattsqcytcy tcwccatact c 21
237 <210> SEQ ID NO: 8
238 <211> LENGTH: 25
239 <212> TYPE: DNA
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: upstream primer used to amplify rpoN gene
245 <400> SEQUENCE: 8
246 ggaacggtag aattctgagc attac 25
248 <210> SEQ ID NO: 9
249 <211> LENGTH: 28
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
254 <223> OTHER INFORMATION: downstream primer used to amplify rpoN gene
256 <400> SEQUENCE: 9
257 ccttttgaat tcgtgcctaa agtaggcg 28
259 <210> SEQ ID NO: 10
260 <211> LENGTH: 222
261 <212> TYPE: PRT
262 <213> ORGANISM: V. harveyi
264 <400> SEQUENCE: 10
265 Ile Gly Ser Ser Gln Thr Met Gln Gln Val Tyr Arg Thr Ile Asp Ser
266 1 5 10 15
267 Ala Ala Ser Ser Lys Ala Ser Ile Phe Ile Thr Gly Glu Ser Gly Thr
268 20 25 30
269 Gly Lys Glu Val Cys Ala Glu Ala Ile His Ala Ala Ser Lys Arg Gly
270 35 40 45
271 Asp Lys Pro Phe Ile Ala Ile Asn Cys Ala Ala Ile Pro Lys Asp Leu
272 50 55 60
273 Ile Glu Ser Glu Leu Phe Gly His Val Lys Gly Ala Phe Thr Gly Ala
274 65 70 75 80
275 Ala Asn Asp Arg Gln Gly Ala Ala Glu Leu Ala Asp Gly Gly Thr Leu
276 85 90 95
277 Phe Leu Asp Glu Leu Cys Glu Met Asp Leu Asp Leu Gln Thr Lys Leu
278 100 105 110
279 Leu Arg Phe Ile Gln Thr Gly Thr Phe Gln Lys Val Gly Ser Ser Lys

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RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\PUNIV.002A.TXT
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 1
Seq#:5; Xaa Pos. 6